

Appendix A



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1gfs

DOI 10.2210/pdb1gfs/pdb

Red - Derived Information

Title GDP-FUCOSE SYNTHETASE FROM E. COLI

Authors Somers, W.S., Stahl, M.L., Sullivan, F.X.

Primary Citation Somers, W.S., Stahl, M.L., Sullivan, F.X. (1998) GDP-fucose synthetase from Escherichia coli: structure of a unique member of the short-chain dehydrogenase/reductase family that catalyzes two distinct reactions at the same active site. *Structure* 6: 1601-1612
[Abstract]

History Deposition 1998-08-17 Release 1999-08-17

Experimental Method Type X-RAY DIFFRACTION Data N/A

Parameters	Resolution[Å]	R-Value	R-Free	Space Group
	2.20	0.171 (obs.)	0.214	P 3 ₂ 2 1
Unit Cell	Length [Å]	a	b	c
	Angles [°]	alpha	beta	gamma
		104.20	104.20	74.90
		90.00	90.00	120.00

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Molecular Description Polymer 1 Molecule GDP-FUCOSE SYNTHETASE Chans A
Asymmetric Unit

Classification Oxidoreductase

Source Polymer 1 Scientific Name Escherichia coli Expression system Escherichia coli

SCOP Classification (version 1.71)	Domain Info	Class	Fold	Superfamily	Family	Domain	Species
d1gfsa_		Alpha and beta proteins (a/b)	NAD(P)-binding Rossmann-fold domains	NAD(P)-binding Rossmann-fold domains	Tyrosine-dependent oxidoreductases	GDP-4-keto-6-deoxy-D-mannose epimerase/reductase Esche (GDP-fucose synthetase)	

CATH Classification (version v3.1.0)	Domain	Class	Architecture	Topology	Homology
1gfsA01		Alpha Beta	3-Layer(aba) Sandwich	Rossmann fold	NAD(P)-bind Rossmann-III
1gfsA02		Alpha Beta	Alpha-Beta Complex	UDP-galactose 4-epimerase; domain 1	UDP-galactose epimerase, d

PFAM Classification	Chain	PFAM Accession	PFAM ID	Description	Type	Clan ID
	A	PF01370	Epimerase	NAD dependent epimerase/dehydratase family	Family	NADP_Rossm

GO Terms	Polymer	Molecular Function	Biological Process	Cellular Component
	GDP-FUCOSE SYNTHETASE (1GFS:A)	<ul style="list-style-type: none">catalytic activitycoenzyme binding	<ul style="list-style-type: none">cellular metabolic process	<ul style="list-style-type: none">none

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